REMARKS

The specification has been amended herein to correct the inadvertent misspellings of *Saccharomyces cerevisiae* due to typographical error.

Claims 1-10, 12, 13 and 16-22 are pending in this application. Claims 4-7, 9 and 16-22 have been withdrawn. Claims 6 and 22 are amended herein to correct the misspelling of *Saccharomyces cerevisiae* due to inadvertent typographical error. Claim 9 has also been amended to correct inadvertent typographical error, replacing a semicolon with a colon in SEQ ID NO: 4, and adding a space in SEQ ID NO: 6. Claim 12 has been amended to improve its readability. New claims 23-25 have been added to complete the record. No new matter is added by these amendments and claims.

Request to Withdraw Finality of Rejections

Applicants had filed a Request to Withdraw Finality of Rejections Under M.P.E.P. § 706.07(d) on November 14, 2006, upon noticing that that final rejection in this case, mailed on October 13, 2006, was premature. Claim 11 was free of prior art rejections in the first Official Action, and Applicants amended claim 1 to incorporate claim 11 in a good-faith effort to narrow the issues. Entry of a new ground of rejection against an originally presented claim after such good-faith reliance is clearly prejudicial to the Applicants.

Because Claim 1 as amended did not substantively alter original Claim 11, Applicants respectfully submitted that the new rejections cannot be based on Applicants' amendment, and therefore the finality of the rejections was premature.

Applicants hereby reiterate their request to withdraw the finality of the rejections contained in this Office Action, and respectfully request that the Examiner reopen the examination of this application, enter the claims and consider the remarks below.

Rejection Under 35 U.S.C. § 112, Second Paragraph

Claims 1-3, 8, 10, 12 and 13 are rejected under 35 U.S.C. § 112, second paragraph, as allegedly indefinite. In Applicants' previous response to this rejection, the Examiner was directed to the meaning of "deleted" as expounded in the specification. The Examiner maintains

that the claims are vague because it is allegedly unclear how a construct comprising only the BC domain can still be termed as an ACCase.

As an initial matter, Applicants note that the disclosure in the specification of an embodiment comprising a construct that only contains the BC domain of ACCase does not limit the invention to this embodiment. As explained in Applicants' previous response, the meaning of "deleted" includes an ACCase containing more of the sequence than the BC domain, but the other domains are rendered non-functional by common molecular biology techniques.

The BC domain found in the claims is not merely a BC domain—it is the BC domain of an ACCase. Furthermore, it is not the mere presence of the BC domain that is claimed. The BC domain as claimed has been manipulated by molecular biology techniques such that the end result is a peptide comprising an ACCase having a deleted biotin binding domain, having a deleted carboxy transferase domain, and having a functional biotin carboxylase domain, wherein said peptide binds to soraphen. Applicants define "functional" with respect to the BC domain of ACCase as binding to soraphen, as pointed out in Applicants' previous response. Applicants provide examples in the specification that show BC domains of ACCase retaining functionality without the ACCase also containing the other two domains normally found in naturally-occurring ACCase.

One skilled in the art would understand the scope of the claims as written. See *Orthokinetics, Inc. v. Safety Travel Chairs, Inc.*, 806 F.2d 1565, 1 USPQ2d 1081 (Fed. Cir. 1986) ("A decision on whether a claim is invalid under § 112, 2d para., requires a determination of whether those skilled in the art would understand what is claimed when the claim is read in light of the specification."). Therefor, the claims are clear as written, and Applicants respectfully request that the rejection under 35 U.S.C. § 112, second paragraph, be withdrawn.

Rejections Under 35 U.S.C. § 102(b)

Bailey et al.

Claims 1-3, 10 and 12 are rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Bailey et al. (1995), Mol. Gen. Genet. 249: 191-201. The Bailey et al. reference describes a probe consisting of a fragment of the coding region of the *U. maydis* ACCase that was used to screen a library and obtain the entire ACCase gene ("ACC1"). That probe happens to correspond

to a small portion of the coding region found in the BC domain of the ACCase gene of *U. maydis*.

In Figure 2, page 193, Bailey et al. compared the deduced amino acid sequences from two possible DNA probes that were amplified by PCR to the corresponding regions of the BC domain of chicken ACCase, yeast PCase, and the alpha subunit of the rat PCCase. Based on this alignment, it was determined that the first DNA fragment, "pUm1," would hybridize to an ACCase, while the second DNA fragment, "pUm2," would not. Therefore pUm1 was used as the probe to obtain the full-length ACCase sequence of *U. maydis* from a genomic libaray.

Bailey et al. in Figure 2 merely aligned the deduced amino acid sequences corresponding to the amplified fragments obtained with degenerate PCR primers in order to determine which amplified fragment would be predicted to be that of an ACCase, and could thus be used to obtain the full sequence of the ACCase in *U. maydis*. The reference was not concerned with actually obtaining a peptide comprising a portion of the BC domain.

Further, even if this peptide could represent a peptide comprising a BC domain, the peptide does not bind to soraphen. The crystal structure of the yeast BC domain bound to soraphen has recently been solved, and the amino acids that interact with soraphen have been determined. In Shen et al., (2004) "A mechanism for the potent inhibition of eukaryotic acetyl-coenzyme A carboxylase by soraphen A, a macrocyclic polyketide natural product," Molecular Cell, 16: 881-891 (enclosed with this Response), the inventors, along with their collaborators at Columbia University, reported the crystal structures of the yeast BC domain, alone and in complex with soraphen. Figure 1 on page 882 shows the residues involved in soraphen binding, highlighted in the figure in green.

The deduced amino acid sequence in Bailey et al. of pUm1 corresponds to amino acids 257-325 of the yeast sequence reported in Shen et al., as demonstrated by the following amino acid sequence alignment:

Sequence # 1 x Sequence # 2 => Protein Alignment

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Protein  sequence        72  aa   LRSGGGKGIRKC ... IFGRDCSVQRRH

  pUm1

Protein  sequence        72  aa   SEGGGGKGIRQV ... LFGRDCSVQRRH

  Yeast ACC
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  Method:           Diagonals (BLOSUM62)
  Layout:           Standard
  Block Length =:   6-aa
  Mismatch penalty: Smaller (1)
  Gap penalty:      Medium  (2)
  Display:          BLOSUM62

                .         20          .         40          .         60
     1 LRSGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAIS 60
       GGGKGIR+    E+F  LY+    E+PGSP+F+MKLAG+ARHLEVQLLADQYG  IS
     1 SEGGGGKGIRQVEREEDFIALYHQAANEIPGSPIFIMKLAGRARHLEVQLLADQYGTNIS 60
                .         20          .         40          .         60
                .
    61 IFGRDCSVQRRH                                                  72
       +FGRDCSVQRRH
    61 LFGRDCSVQRRH                                                  72
                .

  % Identity =  68.1 (49/72)       % Homology =  11.1 (8/72)       % Total =  79.2 (57/72)
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None of the amino acids contained in pUm1 from Bailey et al. are involved in binding soraphen. Thus the claimed peptide is functionally different from the peptide found in Figure 2 of Bailey et al., as evidenced by Shen et al.

Accordingly, because Bailey et al. fails to teach the claimed invention, it is respectfully requested that this rejection be withdrawn.

Schulte et al.

Claims 1-2, 10 and 12 are rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Schulte et al., (1997) Proc. Natl. Acad. Sci. 94: 3465-3470. In Figure 5, Schulte et al. show a "[d]endrogram based on a comparison of deduced amino acid sequences covering the BC domains or BC subunits from ACCases of different organisms" in order to compare the 3 genomic ACCase clones they had isolated from *Brassica napus* (rapeseed plant) to BC sequences that were similar to the BC subunit found in *E. Coli*. Included in the dendrogram is the yeast ACCase BC domain, taken from reference number 50, which is: Al-Feel et al., (1992) "Cloning of the yeast *FAS3* gene and primary structure of yeast acetyl-CoA carboxylase," Proc. Natl. Acad. Sci. 89: 4534-4538.

As an initial matter, Applicants refer to the previous Office Action of May 10, 2006, which states on page 4 that Applicants' election of SEQ ID: 2 (*Ustilago*) would not be treated by

the Examiner as an election of species. In the current Office Action, the Examiner's use of the Schulte et al. reference, which refers to a yeast ACCase, indicates that the Examiner has treated Applicants' election of SEQ ID: 2 as a species election, because the Examiner performed a search that included the yeast ACCase. Furthermore, the "art made of record and not relied upon in any of the rejections" listed on page 7 of the Office Action refers to references of the yeast ACCase, the *Myxococcus xanthus* ACCase, and the *E. Coli* ACCase, also indicating that the Examiner has not limited the examination of this application to the *Ustilago* ACCase. Applicants respectfully request that the Examiner continue to treat Applicants' election of SEQ ID: 2 as a species election.

In the Al-Feel et al. reference, the yeast *FAS3* gene was cloned, the nucleotide sequence of the entire gene was reported, and the *putative* BC domain within the gene was determined, based solely on *deduced* amino acid sequence comparison with ACCase from rat and chicken (page 4534, first column, third paragraph). Importantly, Al-Feel et al. also reported the gene having a putative Biotin Binding ("Biotin Binding Site") and a Carboxytransferase ("Transcarboxylase") domain. Therefore, Al-Feel did not teach of an ACCase having a deleted Biotin Binding domain and deleted Carboxytransferase domain.

The Schulte et al. reference studied the gene sequences of 3 genomic ACCase clones that were isolated from *Brassica napus* (rapeseed plant). These clones differed in their 5' coding regions, and were described as falling into two classes: "one class with an additional 5' exon in the coding region of two ACCase genes and another class represented by one gene that lacks the 5' coding exon and contains an intron in the 5' untranslated region." (Discussion, page 3468). The additional 5' exon was thought to be a putative transit peptide that targets the isoform to the plastids as opposed to the cytosol of the plant. Because these clones differed in their 5' coding regions, Schulte et al. compared the "deduced amino acid sequences covering the BC domain of the three rapeseed ACCases with those from multi-functional ACCases of other organisms as well as those of Escherichis coli and tobacco BC subunits from prokaryotic-type ACCases," which coding region is located at the 5' end of the clones (Discussion, page 3469, left column, first full paragraph). The focus of Schulte et al. on the 5' end of the clones was to look for the presence of the transit peptide in other clones from other organisms, and determine the similarity

of the isolated rapeseed clones with the sequences found at the 5' end of the ACCases of other organisms (Discussion, page 3469, left column, first full paragraph).

There is no discussion or suggestion in Schulte et al. of an ACCase having a deleted biotin binding domain and deleted carboxytransferase domain. Schulte et al. merely studied the 5' portion of the ACCase coding region because the clones that they had isolated from rapeseed differed in that portion of the putative transcripts. Accordingly, Schulte et al. fails to teach the limitations found in Applicants' claims, and Applicants respectfully request that the rejection based on Schulte et al. be withdrawn.

Rejections Under 35 U.S.C. § 103(a)

Claims 1-3, 10, 12 and 13 are rejected under 35 U.S.C. § 103(a) as allegedly unpatentable over Bailey et al. or Schulte et al. in view of Trubetskoy et al., U.S. Pat. 7,098,032. As described above, neither Bailey et al. nor Schulte et al. teach Applicants' invention as claimed, because neither contains all of the elements found in Applicants' claims. Therefore, a combination of references containing either or both Bailey et al. and Schulte et al. with Trubetskoy et al., which was only used by the Examiner to allege a teaching of the pH range found in Applicants' claim 13, cannot support a rejection under § 103(a). Accordingly, Applicants respectfully request that this rejection be withdrawn.

Conclusion

In view of the remarks presented herein, Applicants respectfully submit that this application is in condition for allowance, which action is respectfully requested.

Respectfully submitted,

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Enclosures:

Shen Y., Volrath S.L., Weatherly S.C., Elich T.D., Tong L. (2004) "A mechanism for the potent inhibition of eukaryotic acetyl-coenzyme A carboxylase by soraphen A, a macrocyclic polyketide natural product," Molecular Cell, 16: 881-891.

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